




EXHIBIT 1: Alignment of Xenopus APC (Query) with Murine APC (Subject)

>  sp|Q61315|APC_MOUSE  Adenomatous polyposis coli protein (Protein APC) (mAPC)
gb|AAB59632.1|  APC
Length=2845

Score = 1357 bits (3512), Expect = 0.0, Method: Composition-based stats.
Identities = 742/861 (86%), Positives = 790/861 (91%), Gaps = 8/861 (0%)

Query	1	MAAASYDQLVKQVEALTMNTNLRQELEDN SNHLTKLETEATNMKEVLKQLQGSIEDEAM	60
		MAAASYDQL+KQVEAL MEN+NLRQELEDN SNHLTKLETEA+NMKEVLKQLQGSIEDE M	
Sbjct	1	MAAASYDQLLKQVEALKMENS NLRQELEDN SNHLTKLETEASNMKEVLKQLQGSIEDETM	60
Query	61	ASSGPIDLLERFKDLNLDSSNIPAGKARPKMSMRSYGSREGSLSGHSGECSPVPVGSFQR	120
		+SG IDLLER K+ NLDS N P K R KMS+RSYGSREGS+S SGECSVPV+GSF R	
Sbjct	61	-TSGQIDLLERLKEFNLD S-NFPGVKLR SKMSLRSYGSREGSVSSRSGECSVPVPMGSFPR	118
Query	121	RGLLNGSRESAGYMEELEKERLLLLIAEHEKEEKEKRWYYAQLQNLTKRIDS LPLTENFSM	180
		R +NGSRES GY+EELEKER LL+A+ +KEEKEK WYYAQLQNLTKRIDS LPLTENFS+	
Sbjct	119	RTFVNGSRESTGYLEEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDS LPLTENFSL	178
Query	181	QTMTRRQLEYEARQIRAAMEEQLGTCQDMEKRVQTRVGKIHQIEEEILRIRQLLQSQA	240
		QTMTRRQLEYEARQIRAAMEEQLGTCQDMEKR Q R+ +I QIE++ILR+RQLLQSQ A	
Sbjct	179	QTMTRRQLEYEARQIRAAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRVRQLLQSQA	238
Query	241	EAAERTPQSKHDAGSRDAEKL PDGQGTSEITASGNVSGSGSSSRADHDTTSMSSNSTY	300
		EA ER+ QS+HDA S +A + +G G +E + + SGQ ++R DH+T SV+SS+ T+	
Sbjct	239	EA-ERSSQSRHDAASHEAGRQHEGHGVAESNTAAS-SSGQSPATRV DHETASVLSSSGTH	296
Query	301	SVPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCIAMRQSGCLPLLIQ	360
		S PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCI+MRQSGCLPLLIQ	
Sbjct	297	SAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQ	356
Query	361	LLHGNDKDSVLLGNSRGSKEARASGSAALDNIHSQPDDKGRGRREIRVLHLLLEQIRAYCE	420
		LLHGNDKDSVLLGNSRGSKEARA SAAL NIIHSQPDDKGRGRREIRVLHLLLEQIRAYCE	
Sbjct	357	LLHGNDKDSVLLGNSRGSKEARARASAAALHNIHSQPDDKGRGRREIRVLHLLLEQIRAYCE	416
Query	421	TCWEWQEAHEQGMDQDKNPMPAPVDHQICPAVCVLMKLSFDEEHRHAMNELGGLQAI AEL	480
		TCWEWQEAHEQGMDQDKNPMPAPV+HQICPAVCVLMKLSFDEEHRHAMNELGGLQAI AEL	
Sbjct	417	TCWEWQEAHEQGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAI AEL	476
Query	481	LQVDCEMYGLINDHYSVTLRRYAGMALTNLTFGDVANKATLC SMKSCMRALVAQLKSESE	540
		LQVDCEMYGL NDHYSVTLRRYAGMALTNLTFGDVANKATLC SMK CMRALVAQLKSESE	
Sbjct	477	LQVDCEMYGLTNDHYSVTLRRYAGMALTNLTFGDVANKATLC SMKMGCMRALVAQLKSESE	536
Query	541	DLQQVIASVLRNLSWRADVNSKKT LREVGSVKALMECALDVKKESTLKS VLSALWNLSAH	600
		DLQQVIASVLRNLSWRADVNSKKT LREVGSVKALMECAL+VKKESTLKS VLSALWNLSAH	
Sbjct	537	DLQQVIASVLRNLSWRADVNSKKT LREVGSVKALMECALEVKKESTLKS VLSALWNLSAH	596

Appl. No. 10/525,621
Amdt. dated October 29, 2007
Reply to Office Action of July 27, 2007

PATENT

Query	601	CTENKADICSVDGALAFVLVSTLTYSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE	660
		CTENKADIC+VDGALAFLV TLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE	
Sbjct	597	CTENKADICAVDGALAFVLVGTLTYSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRE	656
Query	661	NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNAKDQEGLDWMGAVSMLKNLIHSHKHKMI	720
		NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARN KDQE LDWMGAVSMLKNLIHSHKHKMI	
Sbjct	657	NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSHKHKMI	716
Query	721	AMGSAAALRNLMANRPAKYKDANIMSPGSSVPSLHVRKQKALEAELDAQHLSETFDNIDN	780
		AMGSAAALRNLMANRPAKYKDANIMSPGSS+PSLHVRKQKALEAELDAQHLSETFDNIDN	
Sbjct	717	AMGSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDN	776
Query	781	LSPKTTNRNKQRHKQNLCSSEYALDSSRHDDSIKSDNFSGNLTVLSPYINTTVLPSSSS	840
		LSPK +HR+KQRHKQNL +YA D++RHDDS RSDNF+ GN+TVLSPY+NTTVLP SSS	
Sbjct	777	LSPKASHRSKQRHKQNLGYAFDANRHDDS--RSDNFNTGNMTVLSPYLNTTVLPSSSS	834
Query	841	PRPTMDGSRPEKDR--ERTAG	859
		R ++D SR EKDR ER G	
Sbjct	835	SRGSLDSSRSEKDRSLERERG	855